

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2003, 05:42:09 : Search time 1720 seconds  
(without alignments) cell updates/sec  
2429,323 Million cell updates/sec

US-09-698-781-3

Scoring table: Oligo

Xgapop 60.0 Xgapext 60.0

Ygapop 60.0 Ygapext 60.0

Fgapop 6.0 Fgapext 7.0

Delop 6.0 Delext 7.0

Searched: 16154066 seqs, 809774376 residues

Word size: 1

Total number of hits satisfying chosen parameters: 341630

Minimum DB seq length: 20

Maximum DB seq length: 99

Post-processing: Listing first 100 summaries

Command line parameters:

-MODEL=frame+P2N\_MODEL -DBV=xlh

-Q=cg12\_1/USP003\_spool/USP003\_spool/runat\_07032003\_083810\_6968/app\_query.fasta\_1.455

-DB=EST -QMT=FastP -SUFFIX=.oli.rst -MINMATCH=0.1 -LOOPC=0 -LOOPEXP=0

-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100

-DOCALIGN=TRUE -THR SCORE=QUALITY -THR MIN=1 -ALIGN=30 -MODE=LOCAL -OUTFMT=pto

-NORMAL = -HEAPSIZE=500 -MINLEN=20 -MAXLEN=99

-USER=US09698781 -EGGN\_1\_1-1906\_0runat\_07032003\_083810\_6968 -NCPU=6 -ICPU=3

-NO\_XLRY - NO\_NMAP - LARGEQUERY -NSG\_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120

-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:\*

1: em\_estba:\*

2: em\_estchum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_espl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hcc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estcom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pin:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_man:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rnd:\*

SUMMARIES

Result No. Score Query Length DB ID Description

1 18 7.0 55 9 AA661880 AA661880 nt95f06.s

2 2 2.7 32 17 A2261946 A2261946 2M023002

3 3 2.7 81 14 B0761111 B0761111 EB004 SO

4 7 2.7 92 14 T89904 T89904 ye1la09.r1

5 5 2.7 92 17 BH38251 BH38251 1008021D0

6 6 2.7 99 9 AA13118 AA13118 zosbell.r

7 7 2.7 31 9 A1142775 A1142775 qax6a20.s

8 6 2.3 32 17 TA318D5P A1197659 T\_brucei

9 6 2.3 35 17 A2238204 A2238204 2M013K17

10 10 2.3 40 9 AA726265 AA726265 vu8pc01.r

11 11 2.3 41 14 H94066 H94066 yy15002.s1

12 12 2.3 41 17 A2813416 A2813416 2M008PM0

13 13 2.3 46 17 A2112916 A2112916 1M018611

14 14 2.3 48 14 C21082 C21082 RUMG000259

15 15 2.3 49 9 AJ281329 AJ281329 ue4te09.r

16 16 2.3 50 9 AJ212979 AJ212979 AU12979

17 17 2.3 50 9 AUI12979 AUI12979

18 18 2.3 51 9 AA616601 AA616601 vn6h08.r

19 19 2.3 51 17 BH218157 BH218157 1006077D0

20 20 2.3 52 17 B00049 B00049 CSRI-10056-

21 21 2.3 52 17 DR15KIT DR15KIT Danio rer

22 22 2.3 57 17 AL758979 AL758979 Arbidiops

23 23 2.3 58 17 A2216082 A2216082 IM0033001

24 24 2.3 59 17 A2213488 A2213488 1M0029008

25 25 2.3 60 17 A2213488 A2213488 1M0029008

26 26 2.3 62 12 BF037661 BF037661 603462102

27 27 2.3 62 17 A220262 A220262 1M0338104

28 28 2.3 63 9 AA761487 AA761487 nz2209.S

29 29 2.3 63 17 AF171487 AF171487 AF219092

30 30 2.3 64 13 B188670 B188670 EST-CD34N

31 31 2.3 64 17 A2479811 A2479811 IM0030116

32 32 2.3 65 17 AL766062 AL766062 Arbidiops

33 33 2.3 66 17 A2231997 A2231997 1M005609

34 34 2.3 66 17 A2617135 A2617135 IM048H13

35 35 2.3 68 17 BH804876 BH804876 1M0010F0

36 36 2.3 69 17 BH638602 BH638602 1M0082D01

37 37 2.3 72 13 BM24830 BM24830 IPSPn0073

38 38 2.3 73 14 R8821 R8821 VP9112.81

39 39 2.3 73 17 BH833910 BH833910 SAK\_0984

40 40 2.3 73 17 BH860880 BH860880 GM\_SI0000

41 41 2.3 73 17 BH862853 BH862853 SALK\_097

42 42 2.3 74 9 AA854584 AA854584 aJ7b03.S

43 43 2.3 74 14 C21414 C21414 HOMG000347

44 44 2.3 75 17 A2206280 A2206280 IM0347B18

45 45 2.3 75 17 A2247788 A2247788 2M0148805

46 46 2.3 75 17 A1762744 A1762744 Arribidops

47 47 2.3 76 9 A1540827 A1540827 tp6812.x

48 48 2.3 76 14 BQ816306 BQ816306 1M030560

49 49 2.3 77 17 A2480476 A2480476 1M0302102

50 50 2.3 78 13 BI517667 BI517667 603042778

51 51 2.3 78 17 BH847206 BH847206 SALK\_0945

52 52 2.3 79 9 A1788666 A1788666 ue656e0.F

53 53 2.3 79 14 BQ094073 BQ094073 048082.32

54 54 2.3 79 14 BQ094091 BQ094091 048082.50

55 55 2.3 79 14 BQ094092 BQ094092 048082.51

56 56 2.3 80 9 AA88157 AA88157 ak22d06.S

57 57 2.3 80 17 CNS01XU7 CNS01XU7 teckradon

58 58 2.3 82 9 AA283715 AA283715 z44qd02.s

59 59 2.3 82 10 AV914126 AV914126

60 60 2.3 83 14 BQ094091 BQ094091 048082.50

61 61 2.3 83 17 BH221159 BH221159 1M0609G0

62 62 2.3 85 9 AJ283196 AJ283196 4A3b-P7G3

63 63 2.3 85 13 B1758902 B1758902 60304252

64 64 2.3 85 17 BH802812 BH802812 10081020

FEATURES	source	Location/Qualifiers	
c 65		1. .55	
c 65		/organism="Homo sapiens"	
c 67		/db_xref="taxon:9606"	
c 68		/clone="IMAGE:206275"	
c 69		/clone.lib="NCI-CGAP_Pri2"	
c 70		/sex="male"	
c 71		/tissue type="metastatic prostate	
c 72		/lbb_host="DHL08"	
c 73		/note="Vector: PAM10; mRNA made from metastatic prostate	
c 74		lesion of the bone, cDNA made by oligo-dT priming.	
c 75		Non-directional cloned. Size-selected on agarose gel,	
c 76		average insert size 600 bp. Library made by D. Krizman,	
c 77		NIN."	
c 78			
c 79			
c 80			
c 81			
c 82			
c 83			
c 84			
c 85			
c 86			
c 87			
c 88			
c 89			
c 90			
c 91			
c 92			
c 93			
c 94			
c 95			
c 96			
c 97			
c 98			
c 99			
c 100			
RESULT 1			
Aa552526			
nK14e0.5			
AW02304	xQ63H626.X		
BQ62486	kd15126.B		
BQ625486	kd15126.B		
A2465721	In027FB10		
A2465721	In027FB10		
A2759336	In0552P21		
Aa87198	Aa87198		
F30846	F30846		
HSP02139 H			
Ak219091	Ak219091		
Ak219050	Tetradec		
Ak9184	Op8d05.s		
AF027915	Af027915		
A1408012	t18pd08.x		
A2921474	A2921474		
Aa22763	Om62ed9.S		
Ak68724	Wk92all.X		
B155724	Bl55724		
B155724	Bl55724		
A2374702	In017J10		
BQ576515	BQ576515		
BQ576515	Sap100L11		
A1764388	A1764388		
A1764388	Aribdops		
AJ281343	AJ281343		
AJ281343	443R-P2C1		
AJ283110	AJ283110		
AJ283110	443A-A-55E1		
AZ941059	AZ941059		
ZN0200108	ZN0200108		
BH612035	BH612035		
SALK_0320	SALK_0320		
A1664297	A1664297		
u88a12.r	u88a12.r		
A1664297	u88a12.r		
A1664297	u88a12.r		
Ak603988	Ak603988		
IM043C08	IM043C08		
Aa012296	Aa012296		
TUBST222	TUBST222		
AV059816	LB7hd22.YG		
BG11920	BG11920		
60222745	60222745		
Az465383	Az465383		
IM02155H14	IM02155H14		
BH244140	BH244140		
1006117A0	1006117A0		
A1883847	A1883847		
tL73e12.x	tL73e12.x		
AB036296	AB036296		
Au177039	Au177039		
Au177039	Au177039		
BQ566189	BQ566189		
9154c07.Y	9154c07.Y		
AL766046	AL766046		
Arabidops	Arabidops		
AL255737	Tetradec		
CNS03QBK	CNS03QBK		
ALIGNMENTS			
BASE COUNT	15 a	NH.. 11 c	
ORIGIN	13 9	16 t	
Alignment Scores:			
Pred. No.:	8.14e-09		
Score:	18.00	Length:	55
Percent Similarity:	100.00%	Matches:	18
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	6.98%	Conservative:	0
DB:	9	Indels:	0
Gaps:	0		
RESULTS			
RESULT 1	OY	188	
Aa661880	GI:261946	GlYAsTlpaLakAxIAlLeuTyVnAlPrTyrgLugGlnG1'AlaProG'sala	
DEFINITION	2M023002R	205	
ACCESSION	2M023002R	mouse 10kb plasmid UGCG2M library Mus musculus genomic	
VERSION	A2961946		
LOCUS	NC_0061946		
SOURCE	GI:13833173		
ORGANISM	Mus musculus		
TITLE			
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCI-CGAP http://www.ncbi.nlm.nih.gov/cicgap.		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., Wright,D., Weiss,R.		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177		
FEATURES	Insert length: 10000 Std Error: 0.00		
source	Plate: 0230 row: O column: 02		
	Seq primer: CACCAAGAACAGCCTATGACCC		
	Class: Plasmid ends		
	High quality sequence stop: 32.		
	Location/Qualifiers		
	1. .32		
	/organism="Mus musculus"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UGCG2M023002"		
	/clone.lib="Mouse 10kb plasmid UGCG2M library"		
	/sex="Female"		
	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-		
	found through the I.M.A.G.E. Consortium/LINX at: www-bio.lnl.gov/bbrp/image.html		
	Trace considered overall poor quality		
	Insert Length: 364 Std Error: 0.00		
	Seq Primer: -0m13 fwd. ET from Amersham		
	High quality sequence stop: 1.		

BASE COUNT	18 a	25 c	26 g	12 t
ORIGIN				
Alignment Scores:				
pred. NO.:	1.1e+03			
Score:	7.00	Length:	81	
percent Similarity:	100.0%	Matches:	7	
best Local Similarity:	100.00%	Conservative:	0	
Query Match:	2.71%	Mismatches:	0	
DB:	14	Indels:	0	
Gaps:	0			
US-09-698-781-3 (1-258) x BQ761111 (1-81)				
Qy 151 HisnythrGlnValValTrp 157				
Db 59 CACTACAGCACAGGTGGTGG 79				
Locus T89904/C				
Locus T89904	92 bp mRNA	Linear	EST	20-MAR-1995
Definition yeast109.r1 Stratagene lung (#937210) Homo sapiens cDNA clone				
Accession T89904				
Version T89904.1	GI:718417			
Keywords EST				
Source human.				
Organism Homo sapiens				
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
Authors 1 (bases 1 to 92)				
Hiller, S., Lennon, G., Becker, M., Donaldson, M.F., Chiappelli, B., Hawkins, .				
Chissoe, S., Dietrich, N., Dubuge, T., Favell, A., Gish, W., Hawkins, .				
N., Huikman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore				
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Ronning, T.,				
Scheibenbogen, K., Soares, J., Tan, F., Merry, M., Trevaskis, E.,				
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.				
Generation and analysis of 280,000 human expressed sequence tags				
Genome Res. 6 (9), 807-828 (1996)				
Title MEDLINE				
Journal 9704478				
Comment Contact: Wilson RK				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
Tel: 314 286 1800				
Fax: 314 286 1810				
Email: est@wustl.edu				
Insert Size: 1079				
High quality sequence stops: 62 Source: IMAGE Consortium, LBL. This				
clone is available royalty-free through LBL; contact the IMAGE				
Consortium (info@image.llnl.gov) for further information.				
Insert Length: 1079 Std Error: 0.00				
Seq primer: M13RPI				
High quality sequence stop: 62.				
Features Location/Qualifiers				
source	1..92			
/organism="Homo sapiens"				
/db_xref="taxon:405689"				
/clone="IMDB:117400"				
/clone_1ib="Stratagene lung (#937210)"				
/sex="male"				
/dev_sturge="72 years"				
/lab host="SOLR cells (kanamycin resistant)"				
/note="organ: lung; Vector: pBlueScript SK(-); Site: 1; ECORI				
/Site_2: XbaI; Cloned unidirectionally; Primer: Oliso				
dr: normal lung. Average insert size: 1.0 kb; Uni-ZAP XR				
Vector: -5' adaptor sequence: 5' GAATTCGCAGCAG 3' -3'				
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTT 3'."				
Base Count	34 a	21 c	24 g	13 t





		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel:	314 286 1800	
	Fax:	314 286 1810	
	Email:	mouseest@wustl.edu	
	This clone is available royalty-free through LILN; contact the	IMAGE Consortium (info@image.lnl.gov) for further information.	
FEATURES	source	MGI:645656	
	Location/Qualifiers	putative full length read	
	1..35	Seq primer: -2dn13 rev1 ET from Amersham	
	/organism="Mus musculus"	High quality sequence stop: 1.	
	/strain="C57BL/6J"	Location/Qualifiers	
	/db_xref="taxon:10090"	1..40	
	/clone="UUGG2M013K17"	Organism="Mus musculus"	
	/clone.lib="Mouse 10kb plasmid UGSC1M library"	/strain="C57BL/6J"	
	/sex="Male"	/db_xref="taxon:10090"	
	/lab_host="E. coli strain XL10-Gold, Tr-resitant, F+	/clone="IMAGE:120312"	
	/clone.lib="Mouse DNA Resource	/clone.lib="Stratagene mouse skin (#937313)"	
	musculus C57BL/6J (male)	/sex="females"	
	was obtained from the Jackson	/tissue-type="whole skin"	
	Laboratory Mouse DNA Resource	/dev-stage="11 weeks old"	
	(http://www.Jax.org/resources/documents/dnares/).	/lab_host="SOXR (kanamycin resistant)"	
	The DNA	/note="Oran: skin; Vector: pBluescript SK-; Site_1: ECORI	
	was hydrodynamically sheared by repeated passage through a	10.5 kb range using preparative agarose gel	
	vector.	Site_2: XbaI; Cloned unidirectionally.	
	The sheared DNA	dr: Whole skin from 11 week old C57BL/6 female mice.	
	was blunt end-repaired with T4 DNA polymerase and T4	Average insert size: 1.0 kb; Uni-ZAP XR vector; -5'	
	polynucleotide kinase. Adaptor oligonucleotides were	adaptor sequence: 5' GATTCGGACG 3' -3' adaptor.	
	ligated to the blunt ends in high molar excess. The		
	adapted DNA was purified and size-selected for a 9.5 to		
	10.5 kb range using preparative agarose gel		
	electrophoresis.		
	Vector DNA was prepared from a derivative		
	of pWV2 (g14732114.gbl AFF2907.1), a copy-number		
	inducible derivative of plasmid RL.		
	The vector was ligated		
	with adaptors complementary to the insert adaptors and		
	purified.		
	The sheared, adapted mouse DNA was annealed to		
	adapted vector DNA, and transformed into chemically-competent		
	E. coli XL10-Gold (Stratagene) cells		
	and selected for ampicillin resistance.		
BASE COUNT	11 a 0 c 24 g 0 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	4.58e+03	Length:	35
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	17	Gaps:	0
US-09-698-781-3 (1-258) x A2838204 (1-35)			
QY	27 LeuLeuProSerPhePro 32		
Db	20 CCGCTTCCCTTCCCT 3		
RESULT 10			
AA726265	AA726265	40 bp mRNA linear EST 02-JAN-1998	
DEFINITION	'u8801.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:12093125 similar to TR:008634 008634 HIGH-SULFUR KERATIN PROTEIN'; mRNA sequence.		
ACCESSION	AA726265		
VERSION	AA726265.1		
KEYWORDS	EST		
SOURCE	house mouse.		
ORGANISM	MUS MUSCULUS		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 40)		
AUTHORS	Marra, M., Hillier, L., Alien, M., Bowles, M., Dierich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schalin-berg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wyllie, R., Lennon, G., Soares, B., Wilson, R., Waterston, R.		
JOURNAL	The WashU-Mouse EST Project		
COMMENT	Unpublished (1995)		
TITLE	Contract: Marra M/Mouse EST Project		
JOURNAL	Washington University School of Medicine		
COMMENT	Washington University School of Medicine		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: mouseest@wustl.edu		
	This clone is available royalty-free through LILN; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	MGI:645656		
	putative full length read		
	Seq primer: -2dn13 rev1 ET from Amersham		
	High quality sequence stop: 1.		
FEATURES	source		
	Location/Qualifiers		
	1..35		
	/organism="Mus musculus"		
	/strain="C57BL/6J"		
	/clone="UUGG2M013K17"		
	/sex="Male"		
	/lab_host="E. coli strain XL10-Gold, Tr-resistant, F+"		
	/clone.lib="Mouse 10kb plasmid UGSC1M library"		
	/note="Male"		
	/lab_host="E. coli strain XL10-Gold, Tr-resistant, F+"		
	/clone.lib="Mouse DNA Resource		
	musculus C57BL/6J (male)		
	was obtained from the Jackson		
	Laboratory Mouse DNA Resource		
	(http://www.Jax.org/resources/documents/dnares/).		
	The DNA		
	was hydrodynamically sheared by repeated passage through a		
	vector.		
	The sheared DNA		
	was blunt end-repaired with T4 DNA polymerase and T4		
	polynucleotide kinase. Adaptor oligonucleotides were		
	ligated to the blunt ends in high molar excess. The		
	adapted DNA was purified and size-selected for a 9.5 to		
	10.5 kb range using preparative agarose gel		
	electrophoresis.		
	Vector DNA was prepared from a derivative		
	of pWV2 (g14732114.gbl AFF2907.1), a copy-number		
	inducible derivative of plasmid RL.		
	The vector was ligated		
	with adaptors complementary to the insert adaptors and		
	purified.		
	The sheared, adapted mouse DNA was annealed to		
	adapted vector DNA, and transformed into chemically-competent		
	E. coli XL10-Gold (Stratagene) cells		
	and selected for ampicillin resistance.		
BASE COUNT	3 a 18 c 11 g 8 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	5.31e+03	Length:	40
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	9	Gaps:	0
US-09-698-781-3 (1-258) x AA726265 (1-40)			
QY	65 AlalValSerProProAla 70		
Db	18 GCAGTGCCCCACCGGCC 35		
RESULT 11			
AA726265	AA726265	41 bp mRNA linear EST 25-NOV-1996	
DEFINITION	'YV15h02.rl Soares fetal liver spleen INF15L Homo sapiens cDNA clone IMAGE:24835 3' similar to gb:Y00493_rnai HEMOCLOSIDN ALPHA CHAIN (HUMAN); mRNA sequence.		
ACCESSION	H94066		
VERSION	YV15h02.rl Soares fetal liver spleen INF15L Homo sapiens cDNA clone IMAGE:24835 3		
KEYWORDS	EST		
SOURCE	EST		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 41)		
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Billiston, K., Hawkins, M., Holman, M., Holtzman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Riffin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.		
JOURNAL	The WashU-Mouse EST Project		
COMMENT	Unpublished (1995)		
	Contact: Wilson RK		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	High quality sequence starts: 1		

Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (<http://image.lnl.gov>) for further information.  
 Trace considered overall poor quality  
 Insert length: 1147 Std Error: 0.00  
 Seq primer: m13 -40 forward  
 Location/Qualifiers

## FEATURES SOURCE

1. .41 /organism="Homo sapiens"  
 /db\_xref="GDB:3791968"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:42835"  
 /clone.lib="Soares fetal liver spleen INFLS"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="DRIHS (ampicillin resistant)"  
 /note="Organ: Liver and Spleen; Vector: pRT3D (Pharmacia)  
 with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 [5' AACGGGAGAATTAAAGACTTCTTTCTTTCTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified pRT3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Ratima Bonaldo."

## BASE COUNT

9 a 9 g 10 g 11 t 2 others

## ORIGIN

## Alignment Scores:

pred. No.:	5.45e+03	Length:	41
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2:338	Indels:	0
DB:	14	Gaps:	0

US-09-698-781-3 (1-258) x H94066 (1-41)

QY 230 LysSerIeuLysLeuThr 235

Db 2 AAGAGCTTGAACTTGACC 19

## RESULT 12

A2813416 LOCUS A2813416 41 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M080M10R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
 ACCESSION A2813416  
 VERSION A2813416.1 GI:12983324  
 KEYWORDS GSS.  
 SOURCE house mouse.

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 41)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Ron 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 1777  
 Email: [dnungegenetics.utah.edu](mailto:dnungegenetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 Row: M Column: 10  
 Seq primer: CACACAGGAACAGCTATGACC

Class: Plasmid ends  
 High quality sequence stop: 41.  
 Location/Qualifiers:  
 1. .41

## FEATURES SOURCE

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCC2K0808N10"  
 /clone.lib="Mouse 10kb plasmid UGCGIM library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="vector: PWD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD2 (9114732141gb) AF129072.1, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." Stratagene)

BASE COUNT

7 a	13 c	8 g	13 t
-----	------	-----	------

ORIGIN

Alignment Scores:

pred. No.:	5.45e+03	Length:	41
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2:334	Indels:	0
DB:	17	Gaps:	0

US-09-698-781-3 (1-258) x A2813416 (1-41)

## QY

231 SerIeuLysLeuThr 236

Db 21 TCGCTCAAGCTGACCTG 38

RESULT 13

LOCUS A2412916	46 bp DNA	linear	GSS 03-OCT-2000
DEFINITION 1M0186J1R Mouse 10kb plasmid UGCGIM library Mus musculus genomic			
ACCESSION A2412916			
VERSION A2412916.1			
KEYWORDS GSS.			
ORGANISM house mouse.			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE 1 (bases 1 to 46)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Ron 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: dunninggenetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0186 row: J column: 11  
 Seq primer: CACAGGAAACGCCATGACC  
 Class: plasmid ends  
 High quality sequence stop: 46.  
 Location/Qualifiers

FEATURES	source
1. . 46	/organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone_id="UUCG1M0186T11" /clone_l1b="Mouse 10kb plasmid UGGCLM library" /sex="Male" /lab_host="B. Coli strain XL10-Gold, Ti-resistant, F-" /note="Vector: Pwd2Inv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.Jax.org/resources/documents/dnares/">http://www.Jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA Polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adaptered DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWd2 (gi 4732114 p AF29072..1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptered mouse DNA was annealed to chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
BASE COUNT	ORIGIN
8 a	9 g 13 t

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1	6.19e+03	46	6	0	0	0	0
2	6.00	46	6	0	0	0	0
3	10.00%	10.00%	0	0	0	0	0
4	Best Local Similarity: 2.33%						

DB: 17

US-09-698-781-3 (1-258) x A2412916 (1-46)

BASE COUNT	ORIGIN
18 a	6 c 9 g 15 t

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1	6.49e+03	48	6	0	0	0	0
2	6.00	48	6	0	0	0	0
3	100.00%	100.00%	0	0	0	0	0
4	Best Local Similarity: 2.33%						

DB: 14

US-09-698-781-3 (1-258) x C21082 (1-48)

QY	Db	RESULT	VERSION	DEFINITION	ACCESSION	KEYWORDS	ORGANISM
27	27	123	A1197659	Soares,mammary_gland_NMLMG mRNA linear EST	A1197659		
LeuLeuProSerPhePro	CRGCTCCCTTCCT	SergInAlleleInSer	14-OCT-1998	IMAGE:494845', similar to TR:Q33563 Q33563	Q33563	EST	
32	44	128		; mRNA sequence.			
		TCACANGCAATCAAGT					
		5					

RESULT 14

C21082/C

LOCUS C21082 48 bp mRNA linear EST 23-OCT-1996

DEFINITION Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA sequence.

ACCESSION C21082

VERSION C21082.1 GI:1622192

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 49)

REFERENCE 1 (bases 1 to 49)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc, T., Geline, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenbach, K., Stoepe, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterson, R.

JOURNAL The WashU-HMMI Mouse EST Project

COMMENT Unpublished (1996)

CONTACT Marra M/Mouse EST Project

Washington University School of Medicine<sup>®</sup>  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu

This clone is available royalty-free through LINC; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

IMAGE ID: 931788

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

	Seq primer: -28nl3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers
FEATURES source	1..49 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:1494184" /clone_1ib="Soares_Mammary_Gland_NMLMG" /sex="Female (lactating)" /tissue_type="mammary gland" /lab_host="DH10B" /note="vector: PTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	19 a 14 c 8 g 8 t 1 others
ORIGIN	OY 10 g 0 t
	Alignment Scores: Pred. No.: 6.64e+03 Length: 49 Score: 6.00 Matches: 6 Percent Similarity: 100.0% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 2.33% Indels: 0 DB: Gaps: 0
RESULT 16	US-09-698-781-3 (1-258) x AT197659 (1-49)
LOCUS	AJ281329 50 bp mRNA linear EST 30-JUN-2000 gambiae cDNA clone 4A3A_P2A7, mRNA sequence.
ACCESSION	AJ281329
VERSION	AJ281329.1 GI:6929210
KEYWORDS	EST.
SOURCE	African malaria mosquito.
ORGANISM	Anopheles gambiae
REFERENCE	Bukayoya; Metzaca; Arthropoda; Hexapoda; Insecta; Pterygota; Neopoda; Endopterygota; Diptera; Nematocera; Culicidae; Anophèles.
AUTHORS	1 (bases 1 to 50) Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C., Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B., and Kafatos,F.C.
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE	20000950
COMMENT	Contact: Dimopoulos G Rotis C. Karafatos Laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany.
FEATURES source	1..50 /organism="Anopheles gambiae" /db_xref="taxon:7165" /clone="4A3A_P2A7" /clone_1ib="Anopheles gambiae immune competent 4A3A" /cell_line="immune competent 4A3A" /lab_host="E. coli DH10B" /note="vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: ECORI; Site_2: NotI; sequenced from
BASE COUNT	1 a 24 c 14 g 11 t
ORIGIN	OY 116 SerSerAlaProSer 121
	forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996). Normalization and Subtraction: Two approaches To facilitate Gene Discovery, Genome Research 6, 791-805.
FEATURES source	Alignment Scores: Pred. No.: 6.79e+03 Length: 50 Score: 6.00 Matches: 6 Percent Similarity: 100.0% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 2.33% Indels: 0 DB: Gaps: 0
BASE COUNT	19 a 14 c 8 g 8 t 1 others
ORIGIN	OY 10 g 0 t
	Alignment Scores: Pred. No.: 6.79e+03 Length: 50 Score: 6.00 Matches: 6 Percent Similarity: 100.0% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 2.33% Indels: 0 DB: Gaps: 0
RESULT 17	US-09-698-781-3 (1-258) x AJ281329 (1-50)
LOCUS	AU102979 50 bp mRNA linear EST 30-AUG-2001 KAT0408, mRNA sequence.
DEFINITION	AU102979 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone AU102979
ACCESSION	AU102979
VERSION	AU102979.1 GI:13552500
KEYWORDS	EST.
ORGANISM	Homo sapiens
REFERENCE	Bukayoya; Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,Y., Nakamura,Y., Sugaya,A. and Sugano,S.
AUTHORS	Diverse transcriptomic initial initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL	MEDLINE 21270072
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Sugaya,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES source	1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="KAT0408" /clone_1ib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
BASE COUNT	1 a 24 c 14 g 11 t
ORIGIN	OY 116 SerSerAlaProSer 121

**Db** 33 |||||||TCCTCCGGCCGTCGCC 50  
**RESULT** 18  
**ACCESSION** AA616601 AA616601  
**DEFINITION** vn66108\_r1 Barstead mouse proximal colon MPLRB6 mRNA linear EST 07-OCT-1997  
**VERSION** AA616601.1 GR:2503806  
**KEYWORDS** EST  
**SOURCE** house mouse.  
**ORGANISM** Mus musculus  
**REFERENCE** 1 (bases 1 to 51)  
**AUTHORS** Marr,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geissel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheibenbogen,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
**TITLE** The WashU-HMM Mouse EST Project  
**JOURNAL** Unpublished (1996)  
**COMMENT** Contact: Marr,M/ Mouse EST Project  
WashU-HMM Mouse EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Fax: 314 286 1810  
Email: mouses@atton.wustl.edu  
This clone is available royalty-free through LBL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
MG157693  
Trace considered overall poor quality  
Seq Primer: -28m13 rev2 ER from Amerham  
High quality sequence stop: 1.  
**FEATURES**  
**source**  
1. .51  
Location/Qualifiers  
/organism="Mus musculus"  
/stain="FVE/N"  
/db\_xref="xaxon:10090"  
/clones="IMAGE:1026207"  
/closure.lib="Barstead mouse proximal colon MPLRB6"  
/dev\_stage="7 day Juvenile"  
/lab\_host="DHL0B"  
/note="Vector: pRT73B-PAC (Pharmacia) with a modified polylinker; Site\_1: EcoRI; Site\_2: NotI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5'-TGTTACGATCGAGGGGGCGCCGTTTGTGTTTCTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCTGATACCTGC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector.  
Library constructed by Bob Barstead.  
**BASE COUNT**  
ORIGIN 10 a 15 c 9 g 17 t  
**BASE COUNT** 9 a 14 c 20 g 8 t  
**ORIGIN**  
**Alignment Scores:**  
**Pred. No.:** 6.94e+03 **Length:** 51  
**Score:** 6.00 **Matches:** 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.33% Indels: 0  
DB: Gaps: 0  
**US-09-698-781-3 (1-258) x AA616601 (1-51)**  
**QY** 27 LeuLeuProSerPhePro 32  
**DB** 25 TGTGACCGCATCCTCCA 42  
**RESULT** 19  
BH21157/c  


---

  
**LOCUS** BH218157 100677D05.2EL.x1 1006 - Rescuemu Grid G zeamays genomic, DNA sequence.  
**ACCESSION** BH218157  
**VERSION** BH218157.1 GI:16810590  
**KEYWORDS** GSS.  
**SOURCE** zeamays.  
**ORGANISM** zeamays  
**REFERENCE** 1 (bases 1 to 51)  
**AUTHORS** Maize genomic sequences found using engineered Rescuemu transposon JOURNAL Unpublished (2001)  
**COMMENT** Contact: Walbot,V  
Department of Biological Sciences  
Stanford University  
185 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1006077 row: 27 Class: transposon/tagged.  
**FEATURES**  
**source**  
1. .51  
Location/Qualifiers  
/organism="Zea mays"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/clones.lib="1006 - Rescuemu Grid G"  
/tissue\_type="Leaf"  
/dev\_stage="adult"  
/lab\_host="DHL0B"  
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site\_1: BamHI; Site\_2: BglII; Rescuemu is a 4.9 kb modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.lastweb.edu' and follow the links for 'rescuemu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DHL0B cells were transformed and then screened on LB plates with ampicillin."  
**BASE COUNT** 9 a 14 c 20 g 8 t  
**ORIGIN**  
**Alignment Scores:**  
**Pred. No.:** 6.94e+03 **Length:** 51  
**Score:** 6.00 **Matches:** 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.33% Indels: 0  
DB: Gaps: 0  
**US-09-698-781-3 (1-258) x BH218157 (1-51)**  
**QY** 117 SerAlaProSerSerTrp 122  
**DB** 37 TCTGACCACTCTCTGG 20  
**RESULT** 20  
B00049  
**LOCUS** B00049 52 bp DNA linear GSS 13-JUL-1996  
**DEFINITION** CSRL-100h6-u CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-100h6, DNA sequence.  
**ACCESSION** B00049  
**VERSION** B00049.1 GI:1409327  
**KEYWORDS** GSS.  
**SOURCE** human.

ORGANISM	Homo sapiens	source	1. .57
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;	/organism="Danio rerio" /db_xref="Taxon:7955"	
REFERENCE	1 (bases 1 to 52)	/clone="Dkey-1k81"	
AUTHORS	Evans,G.A., Burbée,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M., Jones,D., Ward,I., Gillian,E., Schlegemann,J., Probst,S., Harris, ,J., DeFord,J., McFarland,J., Burzinskis,K., Khan,M., Kupfer,K. and Garner,B.R.	/note="Vector PindigoBAC-536"	
TITLE	Genomic Sequence Sampled Map of Chromosome 11	BASE COUNT	11 a 17 c 12 g 17 t
JOURNAL	Unpublished (1996)	ORIGIN	
COMMENT	Contact: Evans GA, Shane Probst McDermott Center for Human Growth and Development University of Texas Southwestern Medical Center At Dallas 5323 Harry Hines Blvd, Dallas TX 75235-0591 Tel: 214-648-1600 Fax: 214-648-1666 Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu	Alignment Scores:	7.85e+03
	Seq primer: T7	Pred. No.:	6.00
	Class: cosmid ends	Score:	100.0%
	High quality sequence stop: 52.	Percent Similarity:	100.0%
FEATURES	Location/Qualifiers	Best Local Similarity:	100.0%
SOURCE	1. .52	Query Match:	2.33%
	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSRL-10h6"	DB:	0
	/clone_lib="CSRL flow sorted Chromosome 11 specific cosmid" /sex="female"	QY	24 ValAlaGlyLeuLeuPro 29
	/clone_type="chimeric hamster somatic cell hybrid" /note="vector: scos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, JI."	Db	44 GTGCCTGACTGCTGCCA 27
BASE COUNT	10 a 6 c 10 g 25 t 1 others	RESULT	22
ORIGIN		ACCESSION	AL758979/c
Alignment Scores:		DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK164B11_013275, genomic survey sequence.
Pred. No.:	7.09e+03	LOCUS	AL758979
Score:	6.00	VERSION	AL758979.1 GI:21497327
Percent Similarity:	100.0%	KEYWORDS	GSS
Best Local Similarity:	100.0%	ORGANISM	Arabidopsis thaliana
Query Match:	2.33%	REVERSE	
DB:	17	REFERENCE	
RESULT	21	A. Rossor, M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics	
DR6KIT/C	DR6KIT	JOURNAL	Unpublished
LOCUS	DR6KIT	REFERENCE	3 (bases 1 to 58)
DEFINITION	Danio rerio genomic clone Dkey-16k1, genomic survey sequence.	AUTHORS	Strizhov,N., Rossor,M., Li,Y. and Weisshaar,B.
ACCESSION	AI733018	TITLE	A pipeline for automated high-throughput generation of ESTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
VERSION	AI733018.1	JOURNAL	Submitted (17-JUN-2002) Weisshaar,B., Max-Planck-Institut fuer Zuechungsforschung, Carl-von-Linne-Weg 10, Koeln, 50620, Germany
KEYWORDS	GSS.	COMMENT	This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atg10820. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is Part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <a href="http://www.mpi-zkoeln.mpg.de/GABI-Kat/">http://www.mpi-zkoeln.mpg.de/GABI-Kat/</a> .
ORGANISM	Danio rerio	FEATURES	1. .58
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cephalopoda; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	SOURCE	/organism="Arabidopsis thaliana" /strain="Columbia 0"
REFERENCE	1 (bases 1 to 57)	/db_xref="taxon:3702"	
AUTHORS	Humphray,S.J., Huckle,E. and Hunt,S.E.	/clone="TK-164B11-03275"	
TITLE	Direct Submission	/clone_lib="Arabidopsis thaliana T-DNA Insertion lines"	
JOURNAL	Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphrey@sanger.ac.uk Unpublished	/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGK161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant	
COMMENT	This sequence was generated from the T7 end of BAC 16k1. 16k1 is part of the Banjokey Pilot BAC Library created by R. Plasterk and N.V. Keygene.	FURTHER DETAILS	<a href="http://www.sanger.ac.uk/projects/D_rerio/">http://www.sanger.ac.uk/projects/D_rerio/</a> .
FEATURES	Location/Qualifiers		

similarity to the *A. thaliana* nuclear genome sequence were processed for submission. T-DNA derived sequences were removed.

BASE COUNT 12 a 10 c 18 g 18 t  
ORIGIN

Alignment Scores:

Pred. No.:	8e+03	Length:	58
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	17	Gaps:	0

US-09-698-781-3 (1-258) x AL758979 (1-58)

QY 37 LYSAPP<sup>O</sup>Alaphether 42  
Db 36 AAGGATCCGGCTTCACA 19

RESULT 23

A2316082/c  
LOCUS A2316082 59 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM003P01R Mouse 10kb plasmid UGCCIM library Mus musculus genomic  
ACCESSION A2316082  
VERSION A2316082.1 GI:10363551  
KEYWORDS GSS.  
ORGANISM Mus musculus  
SOURCE house mouse.

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 59)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D., Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D., Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A.

TITLE

Plasmid Inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 Row: p Column: 01

Seq primer: CACAGGAGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 59.

Location/Qualifiers

1. .59

/organism="Mus musculus"

/strain="C5BL/6J"

/db\_xref="taxon:10090"

/clone="UGCCIM003P01"

/clone\_id="Mouse 10kb plasmid UGCCIM library"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-

/note="vector: PWD2nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnars/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T DNA Polymerase and T4

polynucleotide kinase. Adapter oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD2 (gi|4732141gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 19 a 14 c 13 g 13 t  
ORIGIN

Alignment Scores:

Pred. No.:	8.15e+03	Length:	59
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.33%	Indels:	0
DB:	17	Gaps:	0

US-09-698-781-3 (1-258) x A2316082 (1-59)

QY 204 CysAlasercisP0ASP 209  
Db 50 TSGCCCTTGTCCTGAT 33

RESULT 24

A2313488/c  
LOCUS A2313488 60 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0029E08R Mouse 10kb plasmid UGCCIM library Mus musculus genomic  
ACCESSION A2313488  
VERSION A2313488.1 GI:10358436  
KEYWORDS GSS.  
ORGANISM Mus musculus  
SOURCE house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 60)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D., Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D., Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid Inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 009 Row: E Column: 08

Seq primer: CACAGGAGAACGCTATGACC

Class: Plasmid ends

High quality sequence stop: 60.

Location/Qualifiers

1. .60

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCCIM0029E08"

/clone\_id="Mouse 10kb plasmid UGCCIM library"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-

/note="vector: PWD2nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnars/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T DNA Polymerase and T4

polynucleotide kinase. Adapter oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

was blunt end-repaired with T4 DNA Polymerase and T4 Polynucleotide Kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD18-T (Takara) (AF129072.). A copy-number inducible derivative of plasmid RL, The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter mouse DNA was annealed to adapter vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene). cells and selected for ampicillin resistance.

## BASE COUNT

23 a

0 c

37 g

0 t

## ORIGIN

Alignment Scores:

pred. No.: 8.3e+03

Score: 6.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.33%

DB: BG099525

Length: 60

Matches: 6

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

SOURCE

Organism: Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

(bases 1 to 62)

REFERENCE

NIH-MGC

http://mgc.nci.nih.gov/

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

VERSION

Unpublished (1999)

KEYWORDS

EST.

COMMENT

Email: cgaps@remail.nih.gov

Tissue Procurement: DCTD/DP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)

DNA Sequencing: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium

http://image.llnl.gov

Plate: LLM608 row: d column: 01

High quality sequence start: 15

High quality sequence stop: 59.

Location/OQualifiers

1. .62

FEATURES

source

/organism="Homo sapiens"

/db\_xref="Taxon:9606"

/clone=IMAGE:3865196"

/clone.lib="NIH-MGC\_66"

/tissue.type="adenocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: ovary; Vector: pCMV-SPORT6; Site-1: NotI;

Site-2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.8 kb.

Library constructed by Life

Technologies.

Seq primer:-40UP from Gibco.

Location/Qualifiers

1. .62

FEATURES

source

/organism="Homo sapiens"

/db\_xref="Taxon:9606"

/clone=IMAGE:4105200"

/clone.lib="NIH-CGAP\_Co7"

/tissue.type="adenocarcinoma (mucinous component)"

/lab\_host="DH10B"

/note="Organ: colon; Vector: pAMP1; mRNA made from colonic

adenocarcinoma; cDNA made by oligo-dT priming;

directionally cloned into UBC sites. Size-selected on

agarose gel, average insert size 300 bp. Primary library.

CDNA Library Preparation: David B. Krizman, Ph.D.

Reference: Krizman et al. (1996) Cancer Research

56:5380-5383.

QY

|||||||

VallejuicePhenylval 24

Db

46 GTATATGTTCTAGTA 29

RESULT

26

BF037661/c

LOCUS

BF037661

DEFINITION

mRNA Sequence.

ACCESSION

BF037661

VERSION

GI:10745972

KEYWORDS

EST.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

(bases 1 to 62)

REFERENCE

NIH-MGC

http://mgc.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps@remail.nih.gov

Tissue Procurement: DCTD/DP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)

DNA Sequencing: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium

http://image.llnl.gov

Plate: LLM608 row: d column: 01

High quality sequence start: 15

High quality sequence stop: 59.

Location/OQualifiers

1. .62

FEATURES

source

/organism="Homo sapiens"

/db\_xref="Taxon:9606"

/clone=IMAGE:3865196"

/clone.lib="NIH-MGC\_66"

/tissue.type="adenocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: ovary; Vector: pCMV-SPORT6; Site-1: NotI;

Site-2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.8 kb.

Library constructed by Life

Technologies.

Seq primer:-40UP from Gibco.

Location/Qualifiers

1. .62

FEATURES

source

/organism="Homo sapiens"

/db\_xref="Taxon:9606"

/clone=IMAGE:4105200"

/clone.lib="NIH-CGAP\_Co7"

/tissue.type="adenocarcinoma (mucinous component)"

/lab\_host="DH10B"

/note="Organ: colon; Vector: pAMP1; mRNA made from colonic

adenocarcinoma; cDNA made by oligo-dT priming;

directionally cloned into UBC sites. Size-selected on

agarose gel, average insert size 300 bp. Primary library.

CDNA Library Preparation: David B. Krizman, Ph.D.

Reference: Krizman et al. (1996) Cancer Research

56:5380-5383.

QY

|||||||

VallejuicePhenylval 24

Db

46 GTATATGTTCTAGTA 29

RESULT

27

BASE COUNT

17 a

16 c

12 g

17 t

ORIGIN

17 a

16 c

12 g

17 t

AZ500262/c  
LOCUS AZ500262  
DEFINITION 1M0338H04R Mouse 10kb Plasmid UGGCIM library Mus musculus genomic  
ACCESSION A0761487  
VERSION A0761487.1 GI:10679897  
KEYWORDS GSS.  
SOURCE house mouse  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 62)  
Dunn, D., Aoyagi, I.A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenon, E., Pedersen, T., Reilly,  
,M., Rose, M., Rose, R., Stokes, R., Linney, A., von Niederhausen, A.,  
and Wright, D. Weiss, R. Whole genome scaffolding with paired end reads from 10kb  
Plasmid inserts  
JOURNAL unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah, 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: daunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 038 Row: H Column: 04  
Seq primer: CACAGGAAACCTATGACC  
Class: Plasmid ends  
High quality sequence stop: 62.  
Location/Qualifiers  
1..62  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/clone="UGCIM0338H04"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold,  $\lambda$ -resistant, F-"  
/note="Vector: pmp42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.Jax.org/resources/documents/dnars/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMP42 (<http://47.121.141.98/AFI29072.1>), a copy-number inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into E. coli XL10-Gold  
chemically competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."  
BASE COUNT 27 a  
ORIGIN 1..c  
Alignment Scores:  
Pred. No.: 8.61e+03 Length: 62  
Score: 6.00 Matches: 6 Conservativeness: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.33% Gaps: 0  
DB: 17  
US-09-698-781-3 (1-258) x AA761487 (1-62)

Qy 27 LeuLeuProSerPhePro 32  
Db 53 CTTCTCCCTCCCT 36  
RESULT 28  
A0761487  
LOCUS AA761487  
DEFINITION n22hb9.s1 NCI\_CGAP\_GCB1 Homo sapiens mRNA clone IMAGE:1286577 3,  
mRNA sequence.  
ACCESSION AA761487  
VERSION AA761487.1 GI:2810417  
EST:  
KEYWORDS human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 63)  
NCl-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
TITLE Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
Email: cgsabs@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the T.I.M.A.G.E. Consortium/LNLM AT:  
[www-3dnl.3dnl.gov/bbrp/Image/Image.html](http://db.3dnl.gov/bbrp/Image/Image.html)  
Insert length: 892 Std Error: 0.00  
Seq primer: -40m13 fwd ET from Amersham  
High quality sequence stop: 61.  
Location/Qualifiers  
1..63  
/organism="Homo sapiens"  
/clone="IMAGE:288377"  
/clone="IMAGE:n22hb9.s1 NCI\_CGAP\_GCB1"  
/tissue\_type="germinal center B cell"  
/lbb\_host=DH10B  
/note="Vector: pRT3D-Pac (Pharmacia) with a modified  
polylinker; site\_1: Site\_I: Site\_2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting ((CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTCATCCATCTGAGTGGGAGGGCGCCATTTTTTTTT-3'  
]. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pRT3 vector. Library  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 17 a  
ORIGIN 14..c  
Alignment Scores:  
Pred. No.: 8.76e+03 Length: 63  
Score: 6.00 Matches: 6 Conservativeness: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.33% Gaps: 0  
DB: 9  
US-09-698-781-3 (1-258) x AA761487 (1-63)  
Qy 27 LeuLeuProSerPhePro 32  
Db 27 TTATTACCCCTCTCCA 44

